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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/964,667

DATE: 10/16/2001  
TIME: 15:24:03

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\10162001\I964667.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: de la Monte, Suzanne  
7 Wands, Jack R.

9 (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
10 Screening Drugs Effective for the Treatment or Prevention  
11 of Alzheimer's Disease

13 (iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

17 (B) STREET: 1100 New York Ave., Suite 600

18 (C) CITY: Washington

19 (D) STATE: DC

20 (E) COUNTRY: USA

21 (F) ZIP: 20005-3934

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/964,667 DV

C--> 31 (B) FILING DATE: 28-Sep-2001

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Esmond, Robert W.

36 (B) REGISTRATION NUMBER: 32,893

37 (C) REFERENCE/DOCKET NUMBER: 0609.4370000

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 202-371-2600

41 (B) TELEFAX: 202-371-2540

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 1442 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: double

50 (D) TOPOLOGY: both

52 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

57 (B) LOCATION: 15..1139

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG CCC AGG CTG GAG TGC 50

63 Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys

64 1 5 10

66 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC 98

67 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser

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68	15	20	25	
70	GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC			146
71	Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys			
72	30	35	40	
74	ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT			194
75	Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe			
76	45	50	55	60
78	CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC			242
79	Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro			
80	65	70	75	
82	TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC			290
83	Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala			
84	80	85	90	
86	CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG			338
87	Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met			
88	95	100	105	
90	TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC			386
91	Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu			
92	110	115	120	
94	CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT			434
95	Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile			
96	125	130	135	140
98	TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG			482
99	Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val			
100	145	150	155	
102	CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG			530
103	Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys			
104	160	165	170	
106	CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC			578
107	His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His			
108	175	180	185	
110	CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG			626
111	His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln			
112	190	195	200	
114	AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC			674
115	Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly			
117	205	210	215	220
119	TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC			722
120	Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser			
121	225	230	235	
123	CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT			770
124	Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe			
125	240	245	250	
127	TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC			818
128	Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile			
129	255	260	265	
131	TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT			866
132	Leu Ile Ser Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
133	270	275	280	

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135 GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT	914
136 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys	
137 285 290 295 300	
139 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG	962
140 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	
141 305 310 315	
143 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC	1010
144 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe	
145 320 325 330	
147 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA	1058
148 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro	
149 335 340 345	
151 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT	1106
152 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr	
153 350 355 360	
155 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT	1159
156 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg	
157 365 370 375	
159 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCA GCCGGCTAAT TTAGATAAAA	1219
161 AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCAGGC TGGTCTCAA CTTCTGGCTT	1279
163 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTAACAGTTACA	1339
165 TCTTATTT AGTACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	1399
167 GTAACAGAGT TCTTTATAA CTTTAAACA AAGCTTAGA GCA	1442

170 (2) INFORMATION FOR SEQ ID NO: 2:

172 (i) SEQUENCE CHARACTERISTICS:

173 (A) LENGTH: 375 amino acids

175 (B) TYPE: amino acid

176 (D) TOPOLOGY: linear

178 (ii) MOLECULE TYPE: protein

180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

182 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile	
183 1 5 10 15	
185 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala	
186 20 25 30	
188 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg	
189 35 40 45	
191 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly	
192 50 55 60	
194 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala	
195 65 70 75 80	
197 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu	
198 85 90 95	
200 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp	
201 100 105 110	
203 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp	
204 115 120 125	
206 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu	
207 130 135 140	
209 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp	

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210	145	150	155	160
212	His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala			
213	165	170	175	
215	Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp			
216	180	185	190	
218	Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser			
219	195	200	205	
221	Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro			
222	210	215	220	
224	Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser			
225	225	230	235	240
227	Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu			
228	245	250	255	
230	Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly			
231	260	265	270	
233	Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly			
234	275	280	285	
236	Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met			
237	290	295	300	
239	Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly			
240	305	310	315	320
242	Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser			
243	325	330	335	
245	Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn			
246	340	345	350	
248	Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp			
249	355	360	365	
251	Ser Gln Thr Pro Asp Leu Arg			
252	370	375		
254	(2) INFORMATION FOR SEQ ID NO: 3:			
256	(i) SEQUENCE CHARACTERISTICS:			
257	(A) LENGTH: 1381 base pairs			
258	(B) TYPE: nucleic acid			
259	(C) STRANDEDNESS: double			
260	(D) TOPOLOGY: both			
262	(ii) MOLECULE TYPE: cDNA			
267	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
269	TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGCCAGG CTGGAGTGCA ATGGCGCAAT	60		
271	CTCAGCTCAC CGCAACCTCC GCCTCCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120		
273	AGTAGCTGGG ATTACAGGCA TGTGACCAC GCTCGGCTAA TTTTGTATTT TTTTTAGTA	180		
275	GAGATGGAGT TAACTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCGACCC TCAGATGATC	240		
277	TCCCGTCTCG GCCTGCCAA AGTGTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC	300		
279	TGCCTGGCTA ATTTTGTTGG TAGAACACAGG GTTCACTGA TGTTGCCCAA GCTGGTCTCC	360		
281	TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCAGTCAGCC	420		
283	GTGCCTGGCC TTTTATTTT ATTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT	480		
285	GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTCAA CTCCTGAGAT CAAGCAATCC	540		
287	TCCTGCCTCA GCCTCCCAAG TAGCTGGAC CAAAGACATG CACCACTACA CCTGGTAATT	600		
289	TTTATTTTA TTTTAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC	660		
291	AGTGGCGCAA TCTGGCTCA CTGCAACCTC TGCCCTCCGG GTTCAAGTTA TTCTCCTGCC	720		

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293	CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCAAG CCTAGCTAAT TTTTTGTAT	780
295	TTTTAGTAGA GATGGGGTTT CACCATGTTG GCCAGGTTGA TCTTGATCTC TTGACCTTGT	840
297	GATCTGCCCTG CCTCGGCCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC	900
299	CTATTTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC	960
301	AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC	1020
303	AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCAACACAC CCCGCTAATT TTTGTATTTT	1080
305	CATTAGAGGC GGGTTTACCA TATTGTCAG GCTGGTCTC AAACCTCTGA CCTCAGGTGA	1140
307	CCCACCTGCC TCAGCCTTCC AAAGTGCCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC	1200
309	GGCTAATTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC	1260
311	TCAAACCTCT GGCTTCAGTC AATCCTCCA AATGAGCCAC AACACCCAGC CAGTCACATT	1320
313	TTTAAACAG TTACATCTT ATTGTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAA	1380
315	C	1381

317 (2) INFORMATION FOR SEQ ID NO: 4:

319 (i) SEQUENCE CHARACTERISTICS:

320 (A) LENGTH: 1418 base pairs  
321 (B) TYPE: nucleic acid  
322 (C) STRANDEDNESS: both  
323 (D) TOPOLOGY: both

325 (ii) MOLECULE TYPE: cDNA

330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

332	TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGCCAGG CTGGAGTGCA ATGGCGCAAT	60
334	CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCC CAGCCTCCCC	120
336	AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTGTATT TTTTTTAGT	180
338	AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT	240
340	CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT	300
342	GGCTAATTGTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCCTGAGCT	360
344	CAAGCAGTCC ACCTGCCTCA GCCTCCAAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC	420
346	TGGCCTTTT ATTGTTTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT	480
349	GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC	540
351	TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAAC TACACCTGGC TAATTTTAT	600
353	TTTTATTGTT ATTGTTTGAA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG	660
355	GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCGAG	720
357	CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTGTT TTGTATTGTT	780
359	AGTAGAGATG GGGTTTCACC ATGTTGCCA GTTGTATGCT AGATCTCTG ACCTTGTGAT	840
361	CTGCCTGCC CCGCCTCCC AAGTGTGGG ATTACAGGAC GTGACGCCA CGCCCGGCC	900
363	TATTTTAAAT TTTGTTGTG TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA	960
365	ATGGCCTAACAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT	1020
367	CAGCCTCCC AGCAGCTGGG ATTACGGGCA CCTGCACCAAC ACCCCGCTAA TTTTTGTATT	1080
369	TTCATTAGAG GCGGGGTTTC ACCATATTG TCAGGCTGGT CTCAAACCTCC TGACCTCAGG	1140
371	TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC	1200
373	CGGCTAATTG GAATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG	1260
375	GTCTCAAAC TCTGGCTTCA TGCAATCTT CCAAATGAGC CACAACACCC AGCCAGTCAC	1320
377	ATTTTAAAC AGTTACATCT TTATTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG	1380
379	AACCTGCAAAT TTCGAGTAGT ACAGAGTCTT TTATAACT	1418

381 (2) INFORMATION FOR SEQ ID NO: 5:

383 (i) SEQUENCE CHARACTERISTICS:

384 (A) LENGTH: 22 base pairs  
385 (B) TYPE: nucleic acid  
386 (C) STRANDEDNESS: single

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/964,667

DATE: 10/16/2001  
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]